OIPE

CRF Errors Corrected by the [redacted] Systems Branch

CRF Processing Date: 6/12/98

Serial Number: 09/090,867

Edited by: _____

Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

ENTERED

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

_____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
                          SEQUENCE LISTING

(1)    General Information:

     (i) APPLICANT: Baumgartner, James W.
                    Farrah, Theresa M.
                    Foster, Donald C.
                    Grant, Frank J.
                    O'Hara, Patrick J.

    (ii) TITLE OF INVENTION: Testis-Specific Receptor

   (iii) NUMBER OF SEQUENCES: 33

    (iv) CORRESPONDENCE ADDRESS:
         (A) ADDRESSEE: ZymoGenetics, Inc.
         (B) STREET: 1201 Eastlake Avenue East
         (C) CITY: Seattle
         (D) STATE: WA
         (E) COUNTRY: USA
         (F) ZIP: 98102

     (v) COMPUTER READABLE FORM:
         (A) MEDIUM TYPE: Floppy disk
         (B) COMPUTER: IBM PC compatible
         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
         (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
         (A) APPLICATION NUMBER:
         (B) FILING DATE:
         (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
         (A) NAME: Parker, Gary E.
         (B) REGISTRATION NUMBER: 31,648
         (C) REFERENCE/DOCKET NUMBER: 95-33

    (ix) TELECOMMUNICATION INFORMATION:
         (A) TELEPHONE: 206-442-6673
         (B) TELEFAX: 206-442-6678
```

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
--> **(A) LENGTH: 1167 base pairs**
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 10..1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GATCCGCCC ATG GCT TTC GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC          48
          Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr
            1               5                  10

TTT CTG ATA AGC ACA ACA TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG        96
Phe Leu Ile Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu
     15                  20                  25

ATA AAA GTT AAC CCT CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC       144
Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr
 30                  35                  40                  45

TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT       192
Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His
                 50                  55                  60

TTT AAG GAA TAC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT       240
Phe Lys Glu Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly
             65                  70                  75

AGT GAA ACA TGG AAG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT       288
Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp
         80                  85                  90

GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA       336
Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu
     95                  100                 105

CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA       384
Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu
110                 115                 120                 125

ACT ACT TAT TGG ATA TCA CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG       432
Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln
                130                 135                 140
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308
309  GAT ATG GAT TGC GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG      480
310  Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp
311              145                 150                 155
312
313  AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC      528
314  Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr
315          160                 165                 170
316
317  TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG      576
318  Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys
319      175                 180                 185
320
321  GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA      624
322  Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser
323  190                 195                 200                 205
324
325  GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG      672
326  Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys
327                  210                 215                 220
328
329  CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA      720
330  Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys
331              225                 230                 235
332
333  CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA      768
334  Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu
335          240                 245                 250
336
337  ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT      816
338  Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys
339      255                 260                 265
340
341  TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT      864
342  Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr
343  270                 275                 280                 285
344
345  GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC      912
346  Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr
347                  290                 295                 300
348
349  CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA      960
350  Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser
351              305                 310                 315
352
353  GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT     1008
354  Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly
355          320                 325                 330
356
357  GAA GAC CTA TCG AAG AAA ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT     1056
358  Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly
359      335                 340                 345
360
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      361
      362
      363   TTC ATC TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG      1104
      364   Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys
      365   350                 355                 360                 365
      366
      367   CCA AAC ACC TAC CCA AAA ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT
      368   1159                                                          1159
      369   Pro Asn Thr Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
      370                 370                 375                 380
      371
--->  372   CCTCTAGA                                                        1167
      373
      374
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/090,867*

DATE: 06/12/98
TIME: 10:31:44

INPUT SET: S26648.raw

Line	Error	Original Text
258	Entered (1167) and Calc. Seq. Length (1112) differ	(A) LENGTH: 1167 base pairs
372	# of Sequences for line conflicts w/ running total	CCTCTAGA